

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 16:29:52 ; Search time 18 Seconds
(without alignments)
248.599 Million cell updates/sec

Title: US-10-613-076-48

Perfect score: 1957

Sequence: 1 MPQWLTPLTCRFLNAPT.....PQPRQQAAGXXCYAENX 341

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 97014 segs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pdb*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pdb*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pdb*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pdb*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pdb*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pdb*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pdb*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pdb*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	744.5	40.1	402	7	US-11-174-150-47
2	189.5	10.2	457	6	US-10-986-501-110
3	180.5	9.7	2439	7	US-11-128-059-76
4	173.5	9.3	721	7	US-11-128-059-88
5	173.5	9.3	897	6	US-10-453-372-208
6	173.5	9.3	931	7	US-11-128-059-86
7	173.5	9.3	1323	7	US-11-128-059-92
8	173.5	9.3	1327	7	US-11-128-059-84
9	173.5	9.3	1416	6	US-11-128-059-4
10	173.5	9.3	1502	6	US-10-453-372-252
11	173.5	9.3	1510	6	US-10-453-372-254
12	173.5	9.3	2458	7	US-11-128-059-94
13	173.5	9.3	2551	6	US-10-453-372-256
14	173.5	9.3	2551	7	US-11-128-059-96
15	173	9.3	353	7	US-11-128-059-90
16	171	9.2	315	6	US-10-453-372-212
17	170	9.2	533	6	US-10-453-372-230
18	170	9.2	533	6	US-10-453-372-232
19	170	9.2	552	6	US-10-453-372-236
20	170	9.2	552	6	US-10-453-372-238
21	170	9.2	552	6	US-10-453-372-240
22	170	9.2	552	6	US-10-453-372-242
23	170	9.2	552	6	US-10-453-372-246
24	170	9.2	552	6	US-10-453-372-250
25	170	9.2	556	6	US-10-453-372-210

ALIGNMENTS

RESULT 1

US-11-174-150-47
Sequence 47, Application US/11174150
Publication No: US20050260714A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50022
CURRENT APPLICATION NUMBER: US/11174,150
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/257,174
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: PCT/US01/11797
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/196,603
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/199,417
PRIOR FILING DATE: 2000-04-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 402
TYPE: PRT
ORGANISM: Homo sapiens
US-11-174-150-47

Query Match 40.1%; Score 744.5; DB 7; Length 402;

Best Local Similarity 46.2%; Pred. No. 1.2e-60;

Matches 158; Conservative 43; Mismatches 104; Indels 37; Gaps 9;

Qy	20	IFHKAQGDPAAS-----HPGPHYLLPPHVEVHSHRGATATLPCVLGTTTPPSY-----KVR	69
Db	36	VWHLVLEGSGSVVVTAPGQ-----VWHRGGTIVLPCRYHYEAAAHGHDGVRK	85
Qy	70	WSK-VEFGELRETLITNGHARGYPLGGRABMRGRHRLDASLVAGVLEDEGRVC	128
Db	86	WTKVDP--LAFTDVFVALGPHQHRFAGSYRABELQDGPGLSLVRNVTLQDYGYEC	143
Qy	129	ELINGIEDSEVALTSLLEGVVFYQPSRGYQFNYYEAKQACEQDGRLATYSQYQAWT	188
Db	144	EVTNELEDDAGWKLDLEGVVFYHPRGRYKLTFAEQRACAEQDGLASAEQLHAAR	203
Qy	189	EGLDWCNAGMLLEGSVYFVLTARAPCGRG-----RPGIRSYGPRDRMRDYY	237

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OM protein - protein search, using sw model

Run on: February 10, 2006, 16:28:10 ; Search time 48 Seconds
(without alignments)
587.342 Million cell updates/sec

Title: US-10-613-076-48
Perfect score: 1857
Sequence: 1 MPGLWLTPTLCRFLNRAFTI.....FGPRPQQAAGXCYAENX 341

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgm2_6/ptodata/1/iaa/5 COMB pep.*
- 2: /cgm2_6/ptodata/1/iaa/6 COMB pep.*
- 3: /cgm2_6/ptodata/1/iaa/H COMB pep.*
- 4: /cgm2_6/ptodata/1/iaa/PCTUS COMB pep.*
- 5: /cgm2_6/ptodata/1/iaa/RE COMB pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857.5	46.2	360	2	US-09-907-794A-213
2	857.5	46.2	360	2	US-09-905-125A-213
3	857.5	46.2	360	2	US-09-902-775A-213
4	857.5	46.2	360	2	US-09-906-700-213
5	857.5	46.2	360	2	US-09-903-603A-213
6	857.5	46.2	360	2	US-09-904-920A-213
7	857.5	46.2	360	2	US-09-909-064-213
8	857.5	46.2	360	2	US-09-905-381A-213
9	857.5	46.2	360	2	US-09-906-618-213
10	857.5	46.2	360	2	US-09-906-646-213
11	857.5	46.2	360	2	US-09-904-462-213
12	857.5	46.2	360	2	US-09-902-736A-213
13	857.5	46.2	360	2	US-09-906-722A-213
14	811.5	43.7	373	2	US-09-949-016-10485
15	799	43.0	355	2	US-09-466-778-9
16	772	41.6	326	1	US-08-225-477B-6
17	772	41.6	326	4	PCT-US95-04353-6
18	576.5	31.0	1257	1	US-08-340-428B-49
19	565	30.4	333	4	US-08-225-477B-4
20	565	30.4	333	4	PCT-US95-04353-4
21	564	30.4	289	2	US-09-466-778-8
22	550	29.6	912	4	PCT-US95-03747-2
23	546.5	29.4	378	1	US-08-225-477B-9
24	546.5	29.4	378	4	PCT-US95-04353-9
25	543	29.2	649	2	US-10-188-495-63
26	543	29.2	671	2	US-10-188-495-61
27	533	28.7	371	1	US-08-225-477B-8

28	533	28.7	371	4	PCT-US95-04353-8
29	529.5	28.5	883	2	US-10-195-970-3
30	529.5	28.5	883	2	US-10-195-970-6
31	528.5	28.5	883	2	US-10-188-495-72
32	522	28.1	2316	2	US-09-949-002-314
33	522	28.1	2415	2	US-09-949-002-398
34	517	27.8	2409	6	5180808-2
35	506.5	27.3	328	1	US-08-225-477B-5
36	506.5	27.3	328	4	PCT-US95-04353-5
37	490	26.4	329	1	US-08-225-477B-3
38	490	26.4	329	4	PCT-US95-04353-3
39	403.5	21.7	908	4	PCT-US95-03747-3
40	384.5	20.7	528	2	US-09-010-147B-20
41	384.5	20.7	528	2	US-10-188-495-71
42	338.5	18.2	98	1	US-08-242-097-4
43	338.5	18.2	98	2	US-09-206-695-4
44	338.5	18.2	98	2	US-09-799-118-4
45	204.5	11.0	275	2	US-09-466-778-12

ALIGNMENTS

RESULT 1

US-09-907-794A-213

Sequence 213, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavrin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-17
CURRENT APPLICATION NUMBER: US/09/907,794A
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

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OM protein - protein search, using sw model

Run on: February 10, 2006, 16:29:01 ; Search time 179 Seconds
(without alignments)
795.977 Million cell updates/sec

Title: US-10-613-076-48
Perfect score: 1857
Sequence: 1 MFGWLTFLCRFLWARTI.....FGFPRPQQAAYGVXCYAENX 341

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1856	99.9	340	4 US-10-112-944-397	Sequence 397, App
2	1855	99.9	341	3 US-09-948-820-48	Sequence 48, Appl
3	1855	99.9	341	5 US-10-613-076-48	Sequence 48, Appl
4	1390	74.9	258	3 US-09-764-853-840	Sequence 840, App
5	1390	74.9	258	4 US-10-091-438-205	Sequence 205, App
6	1348	72.6	261	3 US-09-764-853-669	Sequence 669, App
7	1348	72.6	261	4 US-10-091-438-144	Sequence 144, App
8	857.5	46.2	360	3 US-09-909-320-213	Sequence 213, App
9	857.5	46.2	360	3 US-09-909-088B-213	Sequence 213, App
10	857.5	46.2	360	3 US-09-905-291A-213	Sequence 213, App
11	857.5	46.2	360	3 US-09-902-853-213	Sequence 213, App
12	857.5	46.2	360	3 US-09-907-824-213	Sequence 213, App
13	857.5	46.2	360	3 US-09-907-841-213	Sequence 213, App
14	857.5	46.2	360	3 US-09-904-011-213	Sequence 213, App
15	857.5	46.2	360	3 US-09-903-640-213	Sequence 213, App
16	857.5	46.2	360	3 US-09-908-093-213	Sequence 213, App
17	857.5	46.2	360	3 US-09-906-742-213	Sequence 213, App
18	857.5	46.2	360	3 US-09-906-838-213	Sequence 213, App
19	857.5	46.2	360	3 US-09-907-613-213	Sequence 213, App
20	857.5	46.2	360	3 US-09-907-942-213	Sequence 213, App
21	857.5	46.2	360	3 US-09-904-859-213	Sequence 213, App
22	857.5	46.2	360	3 US-09-909-204-213	Sequence 213, App
23	857.5	46.2	360	3 US-09-904-820-213	Sequence 213, App
24	857.5	46.2	360	3 US-09-904-786-213	Sequence 213, App
25	857.5	46.2	360	3 US-09-906-646-213	Sequence 213, App
26	857.5	46.2	360	3 US-09-906-700-213	Sequence 213, App
27	857.5	46.2	360	3 US-09-903-786-213	Sequence 213, App

28	857.5	46.2	360	3 US-09-902-903-213	Sequence 213, App
29	857.5	46.2	360	3 US-09-903-749A-213	Sequence 213, App
30	857.5	46.2	360	3 US-09-904-119-213	Sequence 213, App
31	857.5	46.2	360	3 US-09-904-956-213	Sequence 213, App
32	857.5	46.2	360	3 US-09-902-736-213	Sequence 213, App
33	857.5	46.2	360	3 US-09-907-794-213	Sequence 213, App
34	857.5	46.2	360	3 US-09-903-943-213	Sequence 213, App
35	857.5	46.2	360	3 US-09-904-462-213	Sequence 213, App
36	857.5	46.2	360	3 US-09-907-925-213	Sequence 213, App
37	857.5	46.2	360	3 US-09-902-692-213	Sequence 213, App
38	857.5	46.2	360	3 US-09-903-520-213	Sequence 213, App
39	857.5	46.2	360	3 US-09-905-056-213	Sequence 213, App
40	857.5	46.2	360	3 US-09-909-064-213	Sequence 213, App
41	857.5	46.2	360	3 US-09-904-553-213	Sequence 213, App
42	857.5	46.2	360	3 US-09-905-381-213	Sequence 213, App
43	857.5	46.2	360	3 US-09-904-485-213	Sequence 213, App
44	857.5	46.2	360	3 US-09-905-348-213	Sequence 213, App
45	857.5	46.2	360	3 US-09-905-088-213	Sequence 213, App

ALIGNMENTS

RESULT 1
US-10-112-944-397
Sequence 397, Application US/10112944
Publication No. US20040048279A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt FL_genes Version 5.0
SEQ ID NO 397
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-397

Query Match 99.9%; Score 1856; DB 4; Length 340;
Best Local Similarity 99.4%; Pred. No. 1.1e-152;
Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OM protein - protein search, using sw model
Run on: February 10, 2006, 16:19:59 ; Search time 203 Seconds
(without alignments)
738.070 Million cell updates/sec

Title: US-10-613-076-48
Perfect score: 1857
Sequence: 1 MFGWLTPLTLCRLLWAFI.....FGFPRPQQAAYGXCYAENX 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1856	99.9	340	8 ADM87304	Adm87304 Human pro
2	1856	99.9	343	6 ABU11635	Abu11635 Human MDD
3	1855	99.9	341	3 AAB12304	Aab12304 Human sec
4	1390	74.9	258	4 AAU18060	Aau18060 Human imm
5	1390	74.9	258	4 ABB10532	Abb10532 Human cdn
6	1390	74.9	258	5 ABP67119	Abp67119 Human pol
7	1390	74.9	258	7 ADB31684	Adb31684 Human nov
8	1348	72.6	261	4 AAU17999	Aau17999 Human imm
9	1348	72.6	261	4 ABB10361	Abb10361 Human cdn
10	1348	72.6	261	5 ABP66948	Abp66948 Human pol
11	1348	72.6	261	7 ADB31623	Adb31623 Human nov
12	1052	56.7	191	8 ADP71273	Adp71273 Human LP2
13	857.5	46.2	360	2 AAY13381	Aay13381 Amino aci
14	857.5	46.2	360	3 ADC78533	Adc78533 Human PRO
15	857.5	46.2	360	4 AAB80249	Aab80249 Human PRO
16	857.5	46.2	360	4 AAU29037	Aau29037 Human PRO
17	857.5	46.2	360	4 AAM38965	Aam38965 Human pol
18	857.5	46.2	360	6 ABUS8413	Abu8413 Human PRO
19	857.5	46.2	360	6 ABU71627	Abu71627 Human PRO
20	857.5	46.2	360	6 ABU87961	Abu87961 Novel hum
21	857.5	46.2	360	6 ABU84276	Abu84276 Human sec
22	857.5	46.2	360	6 ABR66150	Abr66150 Human sec
23	857.5	46.2	360	6 ABR65540	Abr65540 Human sec
24	857.5	46.2	360	6 ABUS99480	Abu99480 Human sec

25	857.5	46.2	360	6 ABUS2719	Abu82719 Human PRO
26	857.5	46.2	360	6 ABUS9840	Abu9840 Novel hum
27	857.5	46.2	360	6 ABU71482	Abu71482 Human PRO
28	857.5	46.2	360	6 ABR68089	Abr68089 Human sec
29	857.5	46.2	360	6 ABUS6142	Abu6142 Novel hum
30	857.5	46.2	360	6 ABUS2573	Abu92573 Human sec
31	857.5	46.2	360	6 ABO08650	Abu08650 Human sec
32	857.5	46.2	360	6 ABO02702	Abu02702 Human sec
33	857.5	46.2	360	6 ABR74856	Abr74856 Human sec
34	857.5	46.2	360	6 ABR94618	Abr94618 Human sec
35	857.5	46.2	360	6 ABUS5591	Abu55591 Human PRO
36	857.5	46.2	360	6 ABUS9751	Abu98751 Novel hum
37	857.5	46.2	360	6 ABUS9766	Abu97966 Novel hum
38	857.5	46.2	360	6 ABUS1672	Abu91672 Novel hum
39	857.5	46.2	360	6 ABUS1928	Abu1928 Human sec
40	857.5	46.2	360	6 ABUS9365	Abu9365 Human PRO
41	857.5	46.2	360	6 ABUS6206	Abu86206 Human sec
42	857.5	46.2	360	6 ABUS67419	Abu67419 Human sec
43	857.5	46.2	360	6 ABUS0447	Abu80447 Human PRO
44	857.5	46.2	360	6 ABO01811	Abu01811 Novel hum
45	857.5	46.2	360	6 ABR99365	Abr99365 Human sec

ALIGNMENTS

RESULT 1
ADM87304
ID ADM87304 standard; protein; 340 AA.
XX
AC ADM87304;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human protein SEQ ID NO:397.
XX
KW respiratory; cytostatic; antiarthritic; antiinflammatory;
KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW chromsome tag; genetic fingerprinting; nutritional supplement; cancer;
KW inflammatory condition; arthritis; inflammatory bowel disease;
KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW graft versus host disease; human.
XX
OS Homo sapiens.
XX
PN WO2004009834-A2.
XX
PD 29-JAN-2004.
XX
PF 19-JUL-2002; 2002WO-US022858.
XX
PR 21-JUL-2001; 2001US-0306971P.
XX
PR 28-MAR-2002; 2002US-00112944.
XX
(NUVE-) NUVELO INC.
XX
PA Tang YT, Yang Y, Wang G, Zhang J, Ren F, Xue A, Wang J;
PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
PI WPI; 2004-143291/14.
XX
DR N-PSDB; ADM87060.
XX
PT New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT versus host disease.
XX
PS Claim 20; SEQ ID NO 397; 591pp; English.
XX
CC The present invention describes an isolated polynucleotide (I): (a)
CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC which encodes a polypeptide with biological activity, where the

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OM protein - protein search, using sw model

Run on: February 10, 2006, 16:23:55 ; Search time 43 Seconds
(without alignments)
763.021 Million cell updates/sec

Title: US-10-613-076-48
Perfect score: 1857
Sequence: 1 MFGWLTPLTLCRFLWAFIT.....FGPRPQQAAYGKCYAENX 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1856	99.9	340	JC7505	brain link protein
2	811.5	43.7	354	LKHU	proteoglycan link
3	799	43.0	355	LKCH	proteoglycan link
4	798	43.0	408	LKR2	proteoglycan link
5	795.5	42.8	354	S04243	proteoglycan link
6	788.5	42.5	354	S04238	proteoglycan link
7	579	31.2	1268	S52781	neurocan - mouse
8	576.5	31.0	1257	S28764	neurocan precursor
9	550	29.6	912	A54423	brevican precursor
10	546.5	29.4	378	I46268	brevican precursor
11	533.5	28.7	3562	A47171	chondroitin sulfate
12	533	28.7	371	A53908	brevican precursor
13	529.5	28.5	883	S49126	brevican precursor
14	528.5	28.5	883	S57653	brevican precursor
15	522	28.1	2415	A39086	aggrecan precursor
16	517	27.8	2409	A60979	aggrecan precursor
17	509	27.4	2132	A55182	aggrecan precursor
18	508	27.4	2327	T42630	aggrecan - bovine
19	506.5	27.3	1643	T14274	versican precursor
20	506.5	27.3	3381	T42389	versican precursor
21	506	27.2	370	S29139	aggrecan - pig (fr
22	503.5	27.1	2397	A55535	versican precursor
23	502	27.0	2124	A28452	proteoglycan core
24	495.5	26.7	2109	I50421	aggrecan precursor
25	357	19.2	1340	A39808	proteoglycan core
26	253.5	13.7	862	S43922	versican - pig-tai
27	204.5	11.0	275	JC6506	tumor necrosis fac
28	203.5	11.0	276	A47290	TSG-6 homolog PS4
29	192.5	10.4	277	A41735	hyaluronate-bindin

30	183.5	9.9	113	2	A55885	chondroitin sulfate
31	170	9.2	1069	2	T42681	hypothetical prote
32	164.5	8.9	101	2	A25165	proteoglycan link
33	125	6.7	943	2	B45082	neurotrophic recep
34	107.5	5.8	468	2	D83218	hypothetical prote
35	104.5	5.6	117	1	LKHU2	ig lambda chain pr
36	104.5	5.6	117	1	S04526	ig lambda chain pr
37	104.5	5.6	120	2	S30528	ig lambda chain v
38	104	5.6	919	2	T32541	unc-5 protein - Ca
39	104	5.6	947	1	B44294	unc-5 protein, lon
40	104	5.6	1694	2	S30065	sialoadhesin - mou
41	102.5	5.5	98	2	S36063	ig lambda chain -
42	102	5.5	1323	2	PN0568	connectin 3B - chi
43	102	5.5	4391	2	A38096	perlecan precursor
44	101	5.4	769	1	QRTGS	secretory componen
45	100	5.4	235	2	S25749	ig lambda chain -

ALIGNMENTS

RESULT 1

JC7505
brain link protein-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C:Accession: JC7505
R:Hirakawa, S.; Ohashi, T.; Su, W.D.; Yoshioka, H.; Murakami, T.; Arata, J.; Ninomiya
Biochem. Biophys. Res. Commun. 276, 982-989, 2000
A:Title: The brain link protein-1 (BRAL1): cDNA cloning, genomic structure, and charac
A:Reference number: JC7505
A:Accession: JC7505
A:Molecule type: mRNA
A:Residues: 1-340 <HIR>
A:Cross-references: UNIPROT:Q9GV7; UNIPARC:UPI00000012R0; DDBJ:AB049054
C:Comment: This protein stabilizes the binding between hyaluronan and brain-specific h
C:Genetics:
A:Gene: bral1
C:Superfamily: proteoglycan link protein; immunoglobulin homology; link protein repeat
C:Keywords: brain; tandem repeat

Query Match	99.9%	Score	1856	DB 2	Length	340			
Best Local Similarity	99.4%	Pred. No.	6.2e-144						
Matches	338	Conservative	0	Mismatches	2	Indels	0	Gaps	0
QY	1	MPGWLTLPTLCRFLWAFITFHKAQDPASHPGPHYLLPPIHEVISHRGATATLPCVLG	60						
DB	1	MPGWLTLPTLCRFLWAFITFHKAQDPASHPGPHYLLPPIHEVISHRGATATLPCVLG	60						
QY	61	TTTPSYKVRWSKVDFGELRETLITLITNGLHARGYGLGGRARMRGRHRLDASLVIAGVRL	120						
DB	61	TTTPSYKVRWSKVDFGELRETLITLITNGLHARGYGLGGRARMRGRHRLDASLVIAGVRL	120						
QY	121	DEBGRYRCBLINGIDESVALTSLGCVVFPQPSRGYQFNYYAKQACEODGRLATY	180						
DB	121	DEBGRYRCBLINGIDESVALTSLGCVVFPQPSRGYQFNYYAKQACEODGRLATY	180						
QY	181	SQLYQAWTEGLDWCNAGLLEGSVRYPLVTARAPCGRGRPGIRSYGPRDRMDRYDAFC	240						
DB	181	SQLYQAWTEGLDWCNAGLLEGSVRYPLVTARAPCGRGRPGIRSYGPRDRMDRYDAFC	240						
QY	241	FTSALAGQVFPVPGBLTSEAHAACRRGAVVAKVGHLYAAWKFSGLDCCDGLADGVS	300						
DB	241	FTSALAGQVFPVPGBLTSEAHAACRRGAVVAKVGHLYAAWKFSGLDCCDGLADGVS	300						
QY	301	RPPIITPPRCGGLDPGVRSGFPRPQQAAYGKCYAEN	340						
DB	301	RPPIITPPRCGGLDPGVRSGFPRPQQAAYGTYCYAEN	340						

RESULT 2

LKHU
proteoglycan link protein precursor [validated] - human

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OM protein - protein search, using sw model

Run on: February 10, 2006, 16:20:24 ; Search time 254 Seconds
(without alignments)
947.186 Million cell updates/sec

Title: US-10-613-076-48
Perfect score: 1857
Sequence: 1 MFGWLTPLTCRLLWFTI.....FGPRPQQAAGXCYAENX 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1856	99.9	340	1 HPLN2_HUMAN	Q9GZV7 homo sapien
2	1856	99.9	340	2 Q5T3J0_HUMAN	Q5T3J0 homo sapien
3	1693.5	91.2	341	1 HPLN2_RAT	Q9esm2 rattus norv
4	1690.5	91.0	341	1 HPLN2_MOUSE	Q9esm3 mus musculu
5	1000	53.9	185	2 Q5T3J1_HUMAN	Q5T3J1 homo sapien
6	895	48.2	386	2 Q48472_TETNG	Q48472 tetraodon n
7	857.5	46.2	360	1 HPLN3_HUMAN	Q96886 homo sapien
8	850.5	45.8	383	2 Q5BJ60_XENTR	Q5BJ60 xenopus tro
9	848	45.7	359	2 Q5RLX6_RAT	Q5RLX6 rattus norv
10	848	45.7	394	2 Q6DC16_XENLA	Q6DC16 xenopus lae
11	837	45.1	359	2 Q7ZX17_XENLA	Q7ZX17 xenopus lae
12	834	44.9	359	1 HPLN3_MOUSE	Q80wm5 mus musculu
13	811.5	43.7	354	1 HPLN1_HUMAN	P10915 homo sapien
14	805.5	43.4	363	2 Q6N4V1_BRARE	P10915 homo sapien
15	799	43.0	355	1 HPLN1_CHICK	Q6N4V1 brachydanio
16	795.5	42.8	354	1 HPLN1_PIG	P07354 gallus gall
17	795	42.8	313	2 Q4SHL5_TETNG	P10859 sus scrofa
18	792.5	42.7	356	1 HPLN1_MOUSE	Q4SHL5 tetraodon n
19	791.5	42.6	354	1 HPLN1_RAT	Q9qps5 mus musculu
20	789.5	42.5	354	1 HPLN1_BOVIN	P03994 rattus norv
21	789	42.5	314	2 Q4SE78_TETNG	P52522 bos taurus
22	788.5	42.5	319	2 Q4SLV7_TETNG	Q4SE78 tetraodon n
23	788.5	42.5	354	1 HPLN1_HORSE	Q4SLV7 tetraodon n
24	768	41.4	400	1 HPLN4_MOUSE	C28381 equus cabal
25	744.5	40.1	402	1 HPLN4_HUMAN	Q80wm4 mus musculu
26	714	38.4	335	2 Q6OH44_BRARE	Q86uw8 homo sapien
27	698	37.6	889	2 Q4RUP0_TETNG	Q6OH44 brachydanio
28	579	31.2	1268	1 CSPG3_MOUSE	Q4RUP0 tetraodon n
29	576.5	31.0	1237	1 CSPG3_RAT	P55066 mus musculu
30	568.5	30.6	1321	1 CSPG3_HUMAN	P55067 rattus norv
31	568.5	30.6	1335	2 Q4LB67_HUMAN	Q14594 homo sapien
					Q4LB67 homo sapien

32	566	30.5	1059	2 Q5ISN4_MACFA	Q5ISN4 macaca fasc
33	565.5	30.5	1321	1 CSPG3_PANTR	Q5ISN4 pan troglod
34	559	30.1	1570	2 Q75Z13_BRARE	Q75Z13 brachydanio
35	556.5	30.0	1290	1 Q9W6B1_CHICK	Q9W6B1 gallus gall
36	550	29.6	912	1 PGCB_BOVIN	Q28062 bos taurus
37	546.5	29.4	417	1 PGCB_FELCA	P41725 felis silve
38	545	29.3	1441	2 Q4S3C4_TETNG	Q4S3C4 tetraodon n
39	543	28.2	671	2 Q5T3I5_HUMAN	Q5T3I5 homo sapien
40	543	29.2	911	1 PGCB_HUMAN	Q969W7 homo sapien
41	543	29.2	911	2 Q5S2I0_HUMAN	Q5S2I0 homo sapien
42	536.5	28.9	883	2 Q8OWT7_MOUSE	Q8OWT7 mus musculu
43	536	28.9	2586	2 Q4RUP1_TETNG	Q4RUP1 tetraodon n
44	533.5	28.7	3562	1 CSPG2_CHICK	Q90953 gallus gall
45	530.5	28.6	850	2 Q59P90_HUMAN	Q59P90 homo sapien

ALIGNMENTS

RESULT 1
HPLN2_HUMAN
ID HPLN2_HUMAN STANDARD; PRT; 340 AA.
AC Q9GZV7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hyaluronan and proteoglycan link protein 2 precursor (Brain link protein 1).
GN Name=HAPLN2; Synonyms=BRAL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RX MEDLINE=20483618; PubMed=11027579; DOI=10.1006/bbrc.2000.3583;
RA Hiraoka S., Ohashi T., Su W.-D., Yoshioka H., Murakami T., Arata J.,
RA Ninomiya Y.;
RT "The brain link protein-1 (BRAL1): cDNA cloning, genomic structure,
RT and characterization as a novel link protein expressed in adult
RT brain";
RL Biochem. Biophys. Res. Commun. 276:982-989(2000).
[2]
TI TISSUE=Brain;
TI NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield J.C., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Mediates a firm binding of versican V2 to hyalurononic
CC acid. May play a pivotal role in the formation of the hyaluronan-
CC associated matrix in the central nervous system (CNS) which
CC facilitates neuronal conduction and general structural
CC stabilization. Binds to hyalurononic acid (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By